



hw-8-2.ST25.txt  
SEQUENCE LISTING

<110> Chandrashekar, Ramaswamy  
Morales, Tony H.

<120> PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF

<130> HW-8-2

<140> 10/054,562

<141> 2002-01-22

<150> 09/812,642

<151> 2001-03-20

<150> 09/323,427

<151> 1999-06-01

<160> 18

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> *Dirofilaria immitis*

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tattgctttc tgtactacac ttattgcatt gtcttattcg attccgggtg acaatgggtg 240  
cgaaggtgag ccagaaattg aatgtggacc aacttcaata acaatcaatt ttaatacacg 300  
taatgcattc gaaggacatg tttatgtgaa aggtctttat gatcaagaag gttgccgtaa 360  
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tactgtggaa attctaaatg ctgatggatg tgctcttgat aaatatattgc taaataattt 840  
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 tataaaagat tactgaataa tgaataagct tttcagaagc tataaaagcg atagaagaag 300  
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 gaaatggtaa taatgacggc agcaatcaat gcaatgctta aaccataaa cattgagaag 540  
 ccaaatggtg acatgcagat tccattttgt actgcagcaa gtattacagg ttgtccatta 600  
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 gatgggggta ttattgctgt tgttggtggt tgttggttgt tgttggttgt tgttgctgca 1740  
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 tat tcg att ccg gtt gac aat ggt gtc gaa ggt gag cca gaa att gaa 96  
 Tyr Ser Ile Pro Val Asp Asn Gly Val Glu Gly Glu Pro Glu Ile Glu  
 20 25 30

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tgt gga cca act tca ata aca atc aat ttt aat aca cgt aat gca ttc 144  
 Cys Gly Pro Thr Ser Ile Thr Ile Asn Phe Asn Thr Arg Asn Ala Phe  
 35 40 45

gaa gga cat gtt tat gtg aaa ggt ctt tat gat caa gaa ggt tgc cgt 192  
 Glu Gly His Val Tyr Val Lys Gly Leu Tyr Asp Gln Glu Gly Cys Arg  
 50 55 60

aat gat gaa ggt gga cgt caa gtt gcc gga att tca ctt cca ttt gat 240  
 Asn Asp Glu Gly Gly Arg Gln Val Ala Gly Ile Ser Leu Pro Phe Asp  
 65 70 75 80

tca tgc aat gtt gcg cgt aca cga tct ctg aat cca cgt ggt att ttt 288  
 Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly Ile Phe  
 85 90 95

gta aca aca act gtt gtc att tcg ttt cat cca tta ttt gtt acc aaa 336  
 Val Thr Thr Thr Val Val Ile Ser Phe His Pro Leu Phe Val Thr Lys  
 100 105 110

gtt gat cgt gca tat cga gta caa tgc ttt tac atg gaa gct gat aaa 384  
 Val Asp Arg Ala Tyr Arg Val Gln Cys Phe Tyr Met Glu Ala Asp Lys  
 115 120 125

aca gtt agt gca cag att gag gta tct gaa atc aca act gct ttt caa 432  
 Thr Val Ser Ala Gln Ile Glu Val Ser Glu Ile Thr Thr Ala Phe Gln  
 130 135 140

act caa att gtc ccg atg cca gta tgc cgt tat gaa att ttg gat ggt 480  
 Thr Gln Ile Val Pro Met Pro Val Cys Arg Tyr Glu Ile Leu Asp Gly  
 145 150 155 160

gga cca acc ggt caa cca gtt caa ttt gct atc att ggt cag cca gtt 528  
 Gly Pro Thr Gly Gln Pro Val Gln Phe Ala Ile Ile Gly Gln Pro Val  
 165 170 175

tat cat aaa tgg aca tgc gat tct gaa acc gtt gat act ttc tgc gcg 576  
 Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe Cys Ala  
 180 185 190

gtt gtc cat tcc tgc ttt gtc gat gat ggt aac ggt gat act gtg gaa 624  
 Val Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Thr Val Glu  
 195 200 205

att cta aat gct gat gga tgt gct ctt gat aaa tat ttg cta aat aat 672  
 Ile Leu Asn Ala Asp Gly Cys Ala Leu Asp Lys Tyr Leu Leu Asn Asn  
 210 215 220

ttg gaa tat cca aca gat tta atg gct ggc caa gaa gct cac gta tac 720  
 Leu Glu Tyr Pro Thr Asp Leu Met Ala Gly Gln Glu Ala His Val Tyr  
 225 230 235 240

aaa tat gcg gat cga tca cag ctt ttc tat caa tgc cag atc agt att 768  
 Lys Tyr Ala Asp Arg Ser Gln Leu Phe Tyr Gln Cys Gln Ile Ser Ile  
 245 250 255

acc att aaa gaa cca aat agc gaa tgt gtt cga cca caa tgt tca gaa 816  
 Thr Ile Lys Glu Pro Asn Ser Glu Cys Val Arg Pro Gln Cys Ser Glu  
 260 265 270

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cca caa gga ttc gga gct gtt aaa aca ggt ggt gcc gca gca aaa cct 864  
Pro Gln Gly Phe Gly Ala Val Lys Thr Gly Gly Ala Ala Ala Lys Pro  
275 280 285

gct gca gct gcg caa ctt cgt tta ctc aag aaa aga tct gca gaa ccg 912  
Ala Ala Ala Ala Gln Leu Arg Leu Leu Lys Lys Arg Ser Ala Glu Pro  
290 295 300

gag aat atc att gat gta cga act gat atc aac acc ctt gaa att agc 960  
Glu Asn Ile Ile Asp Val Arg Thr Asp Ile Asn Thr Leu Glu Ile Ser  
305 310 315 320

gat gat aat caa gct ttg cca gtt gat tta cgt cac cgt gca ctt ctg 1008  
Asp Asp Asn Gln Ala Leu Pro Val Asp Leu Arg His Arg Ala Leu Leu  
325 330 335

caa cat aat gga caa cct gta ata ctt gct gca gta caa aat gga atc 1056  
Gln His Asn Gly Gln Pro Val Ile Leu Ala Ala Val Gln Asn Gly Ile  
340 345 350

tgc atg tca cca ttt ggc ttc tca atg ttt atg ggt tta agc att gca 1104  
Cys Met Ser Pro Phe Gly Phe Ser Met Phe Met Gly Leu Ser Ile Ala  
355 360 365

ttg att gct gcc gtc att att acc att tcg ttt aaa ttt cgt cca aat 1152  
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<213> *Dirofilaria immitis*

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20 25 30

Cys Gly Pro Thr Ser Ile Thr Ile Asn Phe Asn Thr Arg Asn Ala Phe  
35 40 45

Glu Gly His Val Tyr Val Lys Gly Leu Tyr Asp Gln Glu Gly Cys Arg  
50 55 60

Asn Asp Glu Gly Gly Arg Gln Val Ala Gly Ile Ser Leu Pro Phe Asp  
65 70 75 80

Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly Ile Phe  
85 90 95

Val Thr Thr Thr Val Val Ile Ser Phe His Pro Leu Phe Val Thr Lys  
100 105 110

Val Asp Arg Ala Tyr Arg Val Gln Cys Phe Tyr Met Glu Ala Asp Lys  
115 120 125

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130 135 140

Thr Gln Ile Val Pro Met Pro Val Cys Arg Tyr Glu Ile Leu Asp Gly  
145 150 155 160

Gly Pro Thr Gly Gln Pro Val Gln Phe Ala Ile Ile Gly Gln Pro Val  
165 170 175

Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe Cys Ala  
180 185 190

Val Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Thr Val Glu  
195 200 205

Ile Leu Asn Ala Asp Gly Cys Ala Leu Asp Lys Tyr Leu Leu Asn Asn  
210 215 220

Leu Glu Tyr Pro Thr Asp Leu Met Ala Gly Gln Glu Ala His Val Tyr  
225 230 235 240

Lys Tyr Ala Asp Arg Ser Gln Leu Phe Tyr Gln Cys Gln Ile Ser Ile  
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Thr Ile Lys Glu Pro Asn Ser Glu Cys Val Arg Pro Gln Cys Ser Glu  
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Pro Gln Gly Phe Gly Ala Val Lys Thr Gly Gly Ala Ala Ala Lys Pro  
275 280 285

Ala Ala Ala Ala Gln Leu Arg Leu Leu Lys Lys Arg Ser Ala Glu Pro  
290 295 300

Glu Asn Ile Ile Asp Val Arg Thr Asp Ile Asn Thr Leu Glu Ile Ser

305

310

320

Asp Asp Asn Gln Ala Leu Pro Val Asp Leu Arg His Arg Ala Leu Leu  
325 330 335

Gln His Asn Gly Gln Pro Val Ile Leu Ala Ala Val Gln Asn Gly Ile  
340 345 350

Cys Met Ser Pro Phe Gly Phe Ser Met Phe Met Gly Leu Ser Ile Ala  
355 360 365

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<213> *Dirofilaria immitis*

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 <213> *Dirofilaria immitis*

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<211> 1372

<212> DNA

<213> *Dirofilaria immitis*

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taaaatctcg aaaccggtaa gaattattga taagatcgaa tagaactatg atttagaatg 180

attattggaa tgaacaagaa aagcggtaaa aaatatgcaa gcaatagcta acatagcacc 240

gaacaaaatg ataagtaaaa tatcatttga tgcaatacag aagataccat tgaattgttc 300

acggctcggt gatgatgata aacgatttgc tgagaagttc ggattctctt cggttatatc 360

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aggacattcg ctatgtggct ctttaattgt tatactaate tggcattgat agtaaagttc 600

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gatcgttcaa cattacacga atccattgcc aattcgattc cagctacctg ccgtccatta 1140

ctatctgaac gacattcatc ctgatcatag agtcctttta catatacgtg tccttcaaata 1200

gtattttctag tattgaaatt gattgttatc gaagctgctc cacattctat ttcagggttca 1260

ccttcgacac cattgtcaat agggatcgat gatacgtagg tcaagtagaa aagtaggaat 1320

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gta tct gaa atg act aca gca ttc caa act caa gtg gta cca atg ccc	96
Val Ser Glu Met Thr Thr Ala Phe Gln Thr Gln Val Val Pro Met Pro	
20 25 30	
gta tgt cga tat gag att ttg gaa ggt gga cca act ggt gca cct gtt	144
Val Cys Arg Tyr Glu Ile Leu Glu Gly Gly Pro Thr Gly Ala Pro Val	
35 40 45	
cga ttt gca atg att gga gat cat gta tat cac aaa tgg aca tgt gat	192
Arg Phe Ala Met Ile Gly Asp His Val Tyr His Lys Trp Thr Cys Asp	
50 55 60	
tca gag act aca gat aca ttc tgt gca tta gta cat tca tgt gtt gtg	240
Ser Glu Thr Thr Asp Thr Phe Cys Ala Leu Val His Ser Cys Val Val	
65 70 75 80	
gat gat gga aaa ggt gat gca gtg gag att ctg aat gaa gaa gga tgt	288
Asp Asp Gly Lys Gly Asp Ala Val Glu Ile Leu Asn Glu Glu Gly Cys	
85 90 95	
gct ttg gac aaa tat tta ctc aat aat ttg gaa tat att aca gat tta	336
Ala Leu Asp Lys Tyr Leu Leu Asn Asn Leu Glu Tyr Ile Thr Asp Leu	
100 105 110	
atg gct ggc caa gaa gct cat gtt tat aaa tat gca gat cga tca gaa	384
Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala Asp Arg Ser Glu	
115 120 125	
ctt tac tat caa tgc cag att agt ata aca att aaa gag cca cat agc	432
Leu Tyr Tyr Gln Cys Gln Ile Ser Ile Thr Ile Lys Glu Pro His Ser	
130 135 140	
gaa tgt cct cga cca caa tgc aca gag cca caa gga ttt ggt gcc ata	480
Glu Cys Pro Arg Pro Gln Cys Thr Glu Pro Gln Gly Phe Gly Ala Ile	
145 150 155 160	
aaa tct gga caa gga ttt gct gct gta aaa tct gct gct gca cca gct	528
Lys Ser Gly Gln Gly Phe Ala Ala Val Lys Ser Ala Ala Ala Pro Ala	
165 170 175	
cca gaa gct tcc ttg ctt tct cca cga ttg atc aag aag cga tca att	576
Pro Glu Ala Ser Leu Leu Ser Pro Arg Leu Ile Lys Lys Arg Ser Ile	
180 185 190	

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Asn Ser Asp Asn Thr Val Asp Val Ser Thr Gly Phe Ser Thr Val Asp  
195 200 205

ata acc gaa gag aat ccg aac ttc tca gca aat cgt tta tca tca tca 672  
Ile Thr Glu Glu Asn Pro Asn Phe Ser Ala Asn Arg Leu Ser Ser Ser  
210 215 220

acg agc cgt gaa caa ttc aat ggt atc ttc tgt att gca tca aat gat 720  
Thr Ser Arg Glu Gln Phe Asn Gly Ile Phe Cys Ile Ala Ser Asn Asp  
225 230 235 240

att tta ctt atc att ttg ttc ggt gct atg tta gct att gct tgc ata 768  
Ile Leu Leu Ile Ile Leu Phe Gly Ala Met Leu Ala Ile Ala Cys Ile  
245 250 255

ttt ttt acc gct ttt ctt gtt cat tcc aat aat cat tct aaa tca 813  
Phe Phe Thr Ala Phe Leu Val His Ser Asn Asn His Ser Lys Ser  
260 265 270

<210> 9

<211> 271

<212> PRT

<213> *Dirofilaria immitis*

<400> 9

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Val Ser Glu Met Thr Thr Ala Phe Gln Thr Gln Val Val Pro Met Pro  
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Val Cys Arg Tyr Glu Ile Leu Glu Gly Gly Pro Thr Gly Ala Pro Val  
35 40 45

Arg Phe Ala Met Ile Gly Asp His Val Tyr His Lys Trp Thr Cys Asp  
50 55 60

Ser Glu Thr Thr Asp Thr Phe Cys Ala Leu Val His Ser Cys Val Val  
65 70 75 80

Asp Asp Gly Lys Gly Asp Ala Val Glu Ile Leu Asn Glu Glu Gly Cys  
85 90 95

Ala Leu Asp Lys Tyr Leu Leu Asn Asn Leu Glu Tyr Ile Thr Asp Leu  
100 105 110

Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala Asp Arg Ser Glu  
115 120 125

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Leu Tyr Tyr Gln Cys Gln Ile Ser Ile Thr Ile Lys Glu Pro His Ser  
130 135 140

Glu Cys Pro Arg Pro Gln Cys Thr Glu Pro Gln Gly Phe Gly Ala Ile  
145 150 155 160

Lys Ser Gly Gln Gly Phe Ala Ala Val Lys Ser Ala Ala Ala Pro Ala  
165 170 175

Pro Glu Ala Ser Leu Leu Ser Pro Arg Leu Ile Lys Lys Arg Ser Ile  
180 185 190

Asn Ser Asp Asn Thr Val Asp Val Ser Thr Gly Phe Ser Thr Val Asp  
195 200 205

Ile Thr Glu Glu Asn Pro Asn Phe Ser Ala Asn Arg Leu Ser Ser Ser  
210 215 220

Thr Ser Arg Glu Gln Phe Asn Gly Ile Phe Cys Ile Ala Ser Asn Asp  
225 230 235 240

Ile Leu Leu Ile Ile Leu Phe Gly Ala Met Leu Ala Ile Ala Cys Ile  
245 250 255

Phe Phe Thr Ala Phe Leu Val His Ser Asn Asn His Ser Lys Ser  
260 265 270

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<211> 813  
<212> DNA  
<213> *Dirofilaria immitis*

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attgaattgt tcacggctcg ttgatgatga taaacgattt gctgagaagt tcggattctc 180  
ttcggttata tcaaccgtgc taaaaccggt actgacgtcc accgtattat cagaattaat 240  
tgatcgcttc ttgatcaatc gtggagaaag caaggaagct tctggagctg gtgcagcagc 300  
agattttaca gcagcaaadc cttgtccaga ttttatggca ccaaatacctt gtggctctgt 360  
gcattgtggc cgaggacatt cgctatgtgg ctctttaatt gttatactaa tctggcattg 420  
atagtaaagt tctgatcgat ctgcatatct ataaacatga gcttcttggc cagccattaa 480

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atctgtaata tattccaaat tattgagtaa atatttgtcc aaagcacatc cttcttcatt 540  
 cagaatctcc actgcatcac cttttccatc atccacaaca catgaatgta ctaatgcaca 600  
 gaatgtatct gtagtctctg aatcacatgt ccatttgtga tatacatgat ctccaatcat 660  
 tgcaaatcga acaggtgcac cagtttgtcc accttccaaa atctcatatc gacatacggg 720  
 cattggtacc acttgagttt ggaatgctgt agtcatttca gataacttcaa ggaccagtac 780  
 taacggtctt atcagctttc catataaaaa cat 813

<210> 11  
 <211> 34  
 <212> DNA  
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<220>  
 <223> Synthetic Primer

<400> 11  
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<210> 12  
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<220>  
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<210> 13  
 <211> 22  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Primer

<400> 13  
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<210> 14  
 <211> 27  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Primer

<400> 14  
 ccatccta atcagactcact atagggc 27

<220>  
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<400> 15
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<210> 16
<211> 892
<212> DNA
<213> Brugia malayi
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<220>
<221> CDS
<222> (158) .. (892)
<223>
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[illegible]

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Tyr	Arg	Leu	Gln	Cys	Phe	Tyr	Met	Glu	Ala	Asp	Lys	Thr	Val	Ser	Thr	
	120					125					130					
caa	att	gaa	gtt	tcc	gaa	atg	aca	acc	gta	ttt	gct	aca	caa	ttg	gta	607
Gln	Ile	Glu	Val	Ser	Glu	Met	Thr	Thr	Val	Phe	Ala	Thr	Gln	Leu	Val	
135					140					145					150	
cca	atg	cct	gtg	tgt	aga	tat	gag	att	ctg	gat	ggg	ggg	cca	acc	gga	655
Pro	Met	Pro	Val	Cys	Arg	Tyr	Glu	Ile	Leu	Asp	Gly	Gly	Pro	Thr	Gly	
				155					160					165		
caa	cct	gtc	cag	tat	gct	aat	att	gga	caa	ccg	gtt	tat	cat	aaa	tgg	703
Gln	Pro	Val	Gln	Tyr	Ala	Asn	Ile	Gly	Gln	Pro	Val	Tyr	His	Lys	Trp	
		170						175					180			
aca	tgt	gat	tct	gaa	aca	gtt	gat	acc	ttc	tgt	gct	ttg	gta	cat	tcc	751
Thr	Cys	Asp	Ser	Glu	Thr	Val	Asp	Thr	Phe	Cys	Ala	Leu	Val	His	Ser	
	185						190					195				
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Cys	Phe	Val	Asp	Asp	Gly	Asn	Gly	Asp	Ser	Ile	Asn	Leu	Ile	Asn	Glu	
	200					205					210					
gaa	gga	tgt	gca	tta	gat	cga	tat	ctt	cta	aat	aat	ttg	gaa	tat	cca	847
Glu	Gly	Cys	Ala	Leu	Asp	Arg	Tyr	Leu	Leu	Asn	Asn	Leu	Glu	Tyr	Pro	
215					220					225					230	
act	gat	cta	atg	gct	ggc	caa	gaa	gct	cac	gta	tac	aaa	tat	gcg		892
Thr	Asp	Leu	Met	Ala	Gly	Gln	Glu	Ala	His	Val	Tyr	Lys	Tyr	Ala		
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<400> 17

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		20						25					30		
Ile	Glu	Cys	Gly	Pro	Thr	Ser	Ile	Thr	Val	Asn	Phe	Asn	Thr	Arg	Asn
		35					40					45			
Pro	Phe	Glu	Gly	His	Val	Tyr	Ala	Lys	Gly	Leu	Tyr	Ser	Asn	Gln	Asp
	50					55					60				

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Cys Arg Ser Asp Glu Gly Gly Arg Gln Val Ala Gly Ile Ser Leu Pro  
65 70 75 80

Phe Asp Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly  
85 90 95

Ile Phe Val Thr Ala Val Val Val Ile Thr Phe His Pro Gln Phe Ile  
100 105 110

Thr Lys Val Asp Arg Thr Tyr Arg Leu Gln Cys Phe Tyr Met Glu Ala  
115 120 125

Asp Lys Thr Val Ser Thr Gln Ile Glu Val Ser Glu Met Thr Thr Val  
130 135 140

Phe Ala Thr Gln Leu Val Pro Met Pro Val Cys Arg Tyr Glu Ile Leu  
145 150 155 160

Asp Gly Gly Pro Thr Gly Gln Pro Val Gln Tyr Ala Asn Ile Gly Gln  
165 170 175

Pro Val Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe  
180 185 190

Cys Ala Leu Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Ser  
195 200 205

Ile Asn Leu Ile Asn Glu Glu Gly Cys Ala Leu Asp Arg Tyr Leu Leu  
210 215 220

Asn Asn Leu Glu Tyr Pro Thr Asp Leu Met Ala Gly Gln Glu Ala His  
225 230 235 240

Val Tyr Lys Tyr Ala  
245

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attgccatca tcaacaaaac aggaatgtac caaagcacag aaggtatcaa ctgtttcaga 180



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 ggttggacca ccatccagaa tctcatatct acacacaggc attggtacca attgtgtagc 300  
 aaatacgggtt gtcatttcgg aaacttcaat ttgtgtgcta acagtcttat cagcttccat 360  
 gtaaaagcat tgcaatcgat atgttcgata aacttttgtg ataaactgtg gatgaaacgt 420  
 aattaccaca acagctgtga caaatattcc acgtggattt aacgaacgtg tacgtgcgac 480  
 attacatgaa tcaaacggta atgatattcc ggctacctga cgtccacctt catcactacg 540  
 acaatcttga ttactgtata atccttttagc atatacatgt ccttcaaaag gatttcgagt 600  
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 attatcaatt ggaatagcat taatacttgc tattatcata tatgacaaaa atgagcaaatt 720  
 ttgcatatgc aacatttaac tttttgcttc tttcttcctg atttcttctc agtgattagt 780  
 gatgaaaata gttggaataa tagaattagc aaaatgatta atttgaaatt gcaacaaatt 840  
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